

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING

### ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,459  
Source: IFWP  
Date Processed by STIC: 1/19/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/553,459

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 ☐ **Use of <220>** Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



do not include these headings. Do not include page numbers.

IFWP

see pp 1-4

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007

TIME: 16:44:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01232007\J553459.raw

see item 4 on  
Error Summary  
Sheet

W--> 1 WO 2004/092396  
W--> 2 PCT/US2004/011622

delete at beginning of the  
file

Does Not Comply  
Corrected Diskette Needed

see item 2  
on Error Summary Sheet

4 <110> APPLICANT: Hallenbeck, Paul  
5 Hampton, Garret  
6 Hay, Carl  
7 Huang, Ying  
8 Jakubczak, John  
9 Phipps, Sandrina

W--> 10 <120> TITLE OF INVENTION: FLAP ENDONUCLEASE 1 (FEN1) REGULATORY SEQUENCES AND USES  
THEREOF

12 <130> FILE REFERENCE: GTIN-021WO

C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/553,459

C--> 14 <141> CURRENT FILING DATE: 2005-10-17

14 <150> PRIOR APPLICATION NUMBER: 60/463,148

15 <151> PRIOR FILING DATE: 2003-04-15

W--> 16 <160> NUMBER OF SEQ ID: 8

17 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Suggestion: Consult  
Sequence  
Rules for  
valid format.

## ERRORED SEQUENCES

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 2259

21 <212> TYPE: DNA

22 <213> ORGANISM: H. sapiens

W--> 23 <400> SEQUENCE: 1

24 catgcgggta tcaagagagcc tgggtgctgcc gtgaaacaga ggctgatttt agcccgga 60

25 tgtagctgca gatcaatggc ccttattagc attttctgag gccataatc tgaccactat 120

26 gaaaacgtga ctaaagggtac gaactctctg cctgagaaaa accacatata agaaaaagtt 180

27 tgctacaat ttccggagct ttgtggacca gtgtctatag acaccaagct gagaaccccc 240

28 gctataagtc actgactggg ggtacccaga tctcaatata tttttttttt gacggagtct 300

29 catttttttg acggcgctctc actctgtctc cggggtgga gggcagtggc acgatctcgg 360

30 ctactgcaa cctctgcctc cggggttcta gagattctca tacctcagcc tctcgagtag 420

31 ctgggactat aggtattacag gtgcgcacca ccacatctaa tttttgtatt tttagtagag 480

32 atgggggttt gccatgctgg ccaggatggg cttgaattcc tgacctcagg tgatctgcct 540

33 gctcgggctt cccaaagtac tgagattaca ggtgtgagtt gccgcgcca ggctcaattt 600

34 tttttttttt ccagacagtc ttgctctatc gccaggtctg gagtgctgg agtgagtgag 660

35 tgccaactcg gctcactgca agctccgctt tctgggttca agtgattatc ctgcctcagc 720

36 ctcccagaca gctgggatta cagggtgtgaa ccaccatgcc cggctaattt tttgtatttt 780

E--> 37 taggagagac aggggtttcac cttgctggcc aggtctggtt tgaacttctg acctctgat 840

38 ccgctcgctt cagcctccca aagtgtctggg attacaggag tgaaccaccg cgctggcccc 900

39 tcaatttcta attcagtatt ttctcacta cctatgctat tatggaatct tgtgagctat 960

E--> 40 ggtcaagaca ttcaagttct ggttctgagt aatctgagtc tgagtaaagc gactgtaata 1020

41 tctatttcac agaactgaaa aataagaaag atgatgaatc aaagcatcta gtgcctagca 1080

Invalid  
nucleic acid  
designators

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007

TIME: 16:44:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01232007\J553459.raw

42 gggagtattt tgctcaacag gtatttgcctt ccttcctaag gctgtaggga agatgatgag 1140  
 E--> 43 ataatgtctt ttatgaaaga gggcctgtaa cgtaaagatc tgtacaaatg ttaacttcat 1200  
 44 tgtcaccggt cagccaatgc ttctaaaatc cagaacataa caactctaga gaagtaaact 1260  
 45 gccccattg ttctgagaca ctggaattca attcagtaaa caatcacggc ccccttcccc 1320  
 46 caaatgata aagacaatca ctgccattta ttgagcttcc aattacgggc cctctgtttg 1380  
 47 gcactgagaa tacaaagatg aatagacatc atcccagagc tagatgcgcg tcagacggtg 1440  
 48 gtcactagga ggcgtggccg aaaacaaaga agtccatgga acgtggccag agatctgtac 1500  
 49 agaggctgtg ggcgctccta ggaaagtctg gccaagtgcc tgagagttgg aagtgttca 1560  
 50 ccaataaaca ttgcccagg gcattgtagg atgggcacgg gttcggcaga agaactttcc 1620  
 51 aaataaagat aacacaccac cgataacaga gatatacaaa ctggaagqta ttcaaaattc 1680  
 E--> 52 ggcgcacgcc tctcgccctt agaaatcgcg agctgagaaa cctaaggagt tcatggcaag 1740  
 53 gggcttcccc ctccccacc cttcagccca agccggaggt tccaggagcg tctagccctc 1800  
 54 tggatctccg gcgtctgagg agataagcgc ggtgtgggtc agaccccgag gggctcctcg 1860  
 E--> 55 atctccgtct ggaactcccc tcaacgctct caccattttg ccccgcaag gctaatccgc 1920  
 56 cgctccgcca ccggaagaac acgtcgacag gagcaggcgc ctagcacaac cggaaaagga 1980  
 57 agtgcctccg gcgcaagtgg cattgagggg cttgtagtcc tgcgatttcg ggtgtagagg 2040  
 58 gagcaggggc ctgcggggac ctggtgtggg tggagtgggg acaagcgggt gagaagggtg 2100  
 E--> 59 1  
 E--> 62 WO 2004/092396  
 E--> 65 Pct/us2004/01162  
 E--> 66 2  
 E--> 69 cgccaggggc gctgagagac tctgttctcc ctggagggac tggttgcat gagagcagcc 2160  
 E--> 70 gtctgagggg acgcagcctg cactacgcgc cccaagaggc tgtgcgtggc gagcagggtca 2220  
 E--> 71 cgtgacggga gcgcgggctt tggaaggcgg ctgaacgctc  
 E--> 72 2259

} invalid

} invalid

delete

see item 1 on Error summary sheet

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:19

FYI

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 71

10/553,459 4

<210> 8  
<211> 270

2

WO 2004/092396

*delete*

PCT/US2004/011  
622

<212> DNA

5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007

TIME: 16:44:19

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01232007\J553459.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:2 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:10 M:283 W: Missing Blank Line separator, <120> field identifier  
L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:283 W: Missing Blank Line separator, <160> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:37 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:40 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:43 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:52 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:55 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:59 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=1  
L:62 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
L:62 M:112 C: (48) String data converted to lower case,  
L:65 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
M:112 Repeated in SeqNo=1  
L:72 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2259 Found:2269 SEQ:1  
L:78 M:283 W: Missing Blank Line separator, <400> field identifier  
L:87 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:103 M:283 W: Missing Blank Line separator, <400> field identifier  
L:109 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:283 W: Missing Blank Line separator, <400> field identifier  
L:119 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:122 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:125 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:126 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:131 M:283 W: Missing Blank Line separator, <400> field identifier